

SEQUENCE LISTING

<110> CARILLO, Serge
BLANCHARD, Jean-Marie
PIECHACZYK, Marc

<120> METHOD OF CANCER TREATMENT BY P53 PROTEIN CONTROL

<130> ST94037A-US

<140>

<141>

<150> 08/737,953

<151> 1996-11-27

<150> FR94/06583

<151> 1994-05-31

<150> WO PCT/FR95/00670

<151> 1995-05-22

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 2085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2085)

<400> 1

atg gaa gga cca cat ctt cct aac aag aaa aaa cac aaa aaa cag gct	48
Met Glu Gly Pro His Leu Pro Asn Lys Lys Lys His Lys Lys Gln Ala	
1 5 10 15	

gta aaa aca gaa cct gag aag aag tca cag tca acc aag ctg tct gtg	96
Val Lys Thr Glu Pro Glu Lys Lys Ser Gln Ser Thr Lys Leu Ser Val	
20 25 30	

gtt cat gag aaa aaa tcc caa gaa gga aag cca aaa gaa cac aca gag	144
Val His Glu Lys Lys Ser Gln Glu Gly Lys Pro Lys Glu His Thr Glu	
35 40 45	

cca aaa agc cta ccc aag cag gca tca gat aca gga agt aac gat gct	192
Pro Lys Ser Leu Pro Lys Gln Ala Ser Asp Thr Gly Ser Asn Asp Ala	
50 55 60	

cac aat aaa aaa gca gtt tcc aga tca gct gaa cag cag cca tca gag	240
His Asn Lys Lys Ala Val Ser Arg Ser Ala Glu Gln Gln Pro Ser Glu	
65 70 75 80	

aaa tca aca gaa cca aag act aaa cca caa gac atg att tct gct ggt	288
Lys Ser Thr Glu Pro Lys Thr Lys Pro Gln Asp Met Ile Ser Ala Gly	

85

90

95

gga gag agt gtt gct ggt atc act gca ata tct ggc aag ccg ggt gac 336
 Gly Glu Ser Val Ala Gly Ile Thr Ala Ile Ser Gly Lys Pro Gly Asp
 100 105 110

aag aaa aaa gaa aag aaa tca tta acc cca gct gtg cca gtt gaa tct 384
 Lys Lys Lys Glu Lys Lys Ser Leu Thr Pro Ala Val Pro Val Glu Ser
 115 120 125

aaa ccg gat aaa cca tcg gga aag tca ggc atg gat gct gct ttg gat 432
 Lys Pro Asp Lys Pro Ser Gly Lys Ser Gly Met Asp Ala Ala Leu Asp
 130 135 140

gac tta ata gat act tta gga gga cct gaa gaa act gaa gaa gaa aat 480
 Asp Leu Ile Asp Thr Leu Gly Gly Pro Glu Glu Thr Glu Glu Glu Asn
 145 150 155 160

aca acg tat act gga cca gaa gtt tca gat cca atg agt tcc acc tac 528
 Thr Thr Tyr Thr Gly Pro Glu Val Ser Asp Pro Met Ser Ser Thr Tyr
 165 170 175

ata gag gaa ttg ggt aaa aga gaa gtc aca att cct cca aaa tat agg 576
 Ile Glu Glu Leu Gly Lys Arg Glu Val Thr Ile Pro Pro Lys Tyr Arg
 180 185 190

gaa cta ttg gct aaa aag gaa ggg atc aca ggg cct cct gca gac tct 624
 Glu Leu Leu Ala Lys Lys Glu Gly Ile Thr Gly Pro Pro Ala Asp Ser
 195 200 205

tca aaa ccc ata ggg cca gat gat gct ata gac gcc ttg tca tct gac 672
 Ser Lys Pro Ile Gly Pro Asp Ala Ile Asp Ala Leu Ser Ser Asp
 210 215 220

ttc acc tgt ggg tcg cct aca gct gct gga aag aaa act gaa aaa gag 720
 Phe Thr Cys Gly Ser Pro Thr Ala Ala Gly Lys Lys Thr Glu Lys Glu
 225 230 235 240

gaa tct aca gaa gtt tta aaa gct cag tca gca ggg aca gtc aga agt 768
 Glu Ser Thr Glu Val Leu Lys Ala Gln Ser Ala Gly Thr Val Arg Ser
 245 250 255

gct gct cca ccc caa gag aag aaa aga aag gtg gag aag gat aca atg 816
 Ala Ala Pro Pro Gln Glu Lys Lys Arg Lys Val Glu Lys Asp Thr Met
 260 265 270

agt gat caa gca ctc gag gct ctg tcg gct tca ctg ggc acc cgg caa 864
 Ser Asp Gln Ala Leu Glu Ala Leu Ser Ala Ser Leu Gly Thr Arg Gln
 275 280 285

gca gaa cct gag ctc gac ctc cgc tca att aag gaa gtc gat gag gca 912
 Ala Glu Pro Glu Leu Asp Leu Arg Ser Ile Lys Glu Val Asp Glu Ala
 290 295 300

aaa gct aaa gaa gaa aaa cta gag aag tgt ggt gag gat gat gaa aca 960
 Lys Ala Lys Glu Glu Lys Leu Glu Lys Cys Gly Glu Asp Asp Glu Thr
 305 310 315 320

atc cca tct gag tac aga tta aaa cca gcc acg gat aaa gat gga aaa Ile Pro Ser Glu Tyr Arg Leu Lys Pro Ala Thr Asp Lys Asp Gly Lys 325 330 335	1008
cca cta ttg cca gag cct gaa gaa aaa ccc aag cct cgg agt gaa tca Pro Leu Leu Pro Glu Pro Glu Glu Lys Pro Lys Pro Arg Ser Glu Ser 340 345 350	1056
gaa ctc att gat gaa ctt tca gaa gat ttt gac cgg tct gaa tgt aaa Glu Leu Ile Asp Glu Leu Ser Glu Asp Phe Asp Arg Ser Glu Cys Lys 355 360 365	1104
gag aaa cca tct aag cca act gaa aag aca gaa gaa tct aag gcc gct Glu Lys Pro Ser Lys Pro Thr Glu Lys Thr Glu Glu Ser Lys Ala Ala 370 375 380	1152
gct cca gct cct gtg tcg gag gct gtg tct cgg acc tcc atg tgt agt Ala Pro Ala Pro Val Ser Glu Ala Val Ser Arg Thr Ser Met Cys Ser 385 390 395 400	1200
ata cag tca gca ccc cct gag ccg gct acc ttg aag ggc aca gtg cca Ile Gln Ser Ala Pro Pro Glu Pro Ala Thr Leu Lys Gly Thr Val Pro 405 410 415	1248
gat gat gct gta gaa gcc ttg gct gat agc ctg ggg aaa aag gaa gca Asp Asp Ala Val Glu Ala Leu Ala Asp Ser Leu Gly Lys Lys Glu Ala 420 425 430	1296
gat cca gaa gat gga aaa cct gtg atg gat aaa gtc aag gag aag gcc Asp Pro Glu Asp Gly Lys Pro Val Met Asp Lys Val Lys Glu Lys Ala 435 440 445	1344
aaa gaa gaa gac cgt gaa aag ctt ggt gaa aaa gaa gaa aca att cct Lys Glu Glu Asp Arg Glu Lys Leu Gly Glu Lys Glu Glu Thr Ile Pro 450 455 460	1392
cct gat tat aga tta gaa gag gtc aag gat aaa gat gga aag cca ctc Pro Asp Tyr Arg Leu Glu Glu Val Lys Asp Lys Asp Gly Lys Pro Leu 465 470 475 480	1440
ctg cca aaa gag tct aag gaa cag ctt cca ccc atg agt gaa gac ttc Leu Pro Lys Glu Ser Lys Glu Gln Leu Pro Pro Met Ser Glu Asp Phe 485 490 495	1488
ctt ctg gat gct ttg tct gag gac ttc tct ggt cca caa aat gct tca Leu Leu Asp Ala Leu Ser Glu Asp Phe Ser Gly Pro Gln Asn Ala Ser 500 505 510	1536
tct ctt aaa ttt gaa gat gct aaa ctt gct gct gcc atc tct gaa gtg Ser Leu Lys Phe Glu Asp Ala Lys Leu Ala Ala Ala Ile Ser Glu Val 515 520 525	1584
gtt tcc caa acc cca gct tca acg acc caa gct gga gcc cca ccc cgt Val Ser Gln Thr Pro Ala Ser Thr Thr Gln Ala Gly Ala Pro Pro Arg 530 535 540	1632
gat acc tcg cag agt gac aaa gac ctc gat gat gcc ttg gat aaa ctc Asp Thr Ser Gln Ser Asp Lys Asp Leu Asp Asp Ala Leu Asp Lys Leu	1680

545	550	555	560	
tct gac agt cta gga caa agg cag cct gac cca gat gag aac aaa cca				1728
Ser Asp Ser Leu Gly Gln Arg Gln Pro Asp Pro Asp Glu Asn Lys Pro	565	570	575	
atg gga gat aaa gta aag gaa aaa gct aaa gct gaa cat aga gac aag				1776
Met Gly Asp Lys Val Lys Glu Lys Ala Lys Ala Glu His Arg Asp Lys	580	585	590	
ctt gga gaa aga gat gac act atc cca cct gaa tac aga cat ctc ctg				1824
Leu Gly Glu Arg Asp Asp Thr Ile Pro Pro Glu Tyr Arg His Leu Leu	595	600	605	
gat gat aat gga cag gac aaa cca gtg aag cca cct aca aag aaa tca				1872
Asp Asp Asn Gly Gln Asp Lys Pro Val Lys Pro Pro Thr Lys Lys Ser	610	615	620	
gag gat tca aag aaa cct gca gat gac caa gac ccc att gat gct ctc				1920
Glu Asp Ser Lys Lys Pro Ala Asp Asp Gln Asp Pro Ile Asp Ala Leu	625	630	635	640
tca gga gat ctg gac agc tgt ccc tcc act aca gaa acc tca cag aac				1968
Ser Gly Asp Leu Asp Ser Cys Pro Ser Thr Thr Glu Thr Ser Gln Asn	645	650	655	
aca gca aag gat aag tgc aag aag gct gct tcc agc tcc aaa gca cct				2016
Thr Ala Lys Asp Lys Cys Lys Lys Ala Ala Ser Ser Ser Lys Ala Pro	660	665	670	
aag aat gga ggt aaa gcg aag gat tca gca aag aca aca gag gaa act				2064
Lys Asn Gly Gly Lys Ala Lys Asp Ser Ala Lys Thr Thr Glu Glu Thr	675	680	685	
tcc aag cca aaa gat gac taa				2085
Ser Lys Pro Lys Asp Asp	690	695		

<210> 2
 <211> 694
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Glu Gly Pro His Leu Pro Asn Lys Lys Lys His Lys Lys Gln Ala
 1 5 10 15
 Val Lys Thr Glu Pro Glu Lys Lys Ser Gln Ser Thr Lys Leu Ser Val
 20 25 30
 Val His Glu Lys Lys Ser Gln Glu Gly Lys Pro Lys Glu His Thr Glu
 35 40 45
 Pro Lys Ser Leu Pro Lys Gln Ala Ser Asp Thr Gly Ser Asn Asp Ala
 50 55 60
 His Asn Lys Lys Ala Val Ser Arg Ser Ala Glu Gln Gln Pro Ser Glu
 65 70 75 80
 Lys Ser Thr Glu Pro Lys Thr Lys Pro Gln Asp Met Ile Ser Ala Gly
 85 90 95
 Gly Glu Ser Val Ala Gly Ile Thr Ala Ile Ser Gly Lys Pro Gly Asp

				100					105					110			
Lys	Lys	Lys	Glu	Lys	Lys	Ser	Leu	Thr	Pro	Ala	Val	Pro	Val	Glu	Ser		
		115					120					125					
Lys	Pro	Asp	Lys	Pro	Ser	Gly	Lys	Ser	Gly	Met	Asp	Ala	Ala	Leu	Asp		
	130					135					140						
Asp	Leu	Ile	Asp	Thr	Leu	Gly	Gly	Pro	Glu	Glu	Thr	Glu	Glu	Glu	Asn		
145					150					155					160		
Thr	Thr	Tyr	Thr	Gly	Pro	Glu	Val	Ser	Asp	Pro	Met	Ser	Ser	Thr	Tyr		
				165					170						175		
Ile	Glu	Glu	Leu	Gly	Lys	Arg	Glu	Val	Thr	Ile	Pro	Pro	Lys	Tyr	Arg		
			180					185					190				
Glu	Leu	Leu	Ala	Lys	Lys	Glu	Gly	Ile	Thr	Gly	Pro	Pro	Ala	Asp	Ser		
	195					200					205						
Ser	Lys	Pro	Ile	Gly	Pro	Asp	Asp	Ala	Ile	Asp	Ala	Leu	Ser	Ser	Asp		
	210					215					220						
Phe	Thr	Cys	Gly	Ser	Pro	Thr	Ala	Ala	Gly	Lys	Lys	Thr	Glu	Lys	Glu		
225					230					235					240		
Glu	Ser	Thr	Glu	Val	Leu	Lys	Ala	Gln	Ser	Ala	Gly	Thr	Val	Arg	Ser		
				245					250						255		
Ala	Ala	Pro	Pro	Gln	Glu	Lys	Lys	Arg	Lys	Val	Glu	Lys	Asp	Thr	Met		
			260					265						270			
Ser	Asp	Gln	Ala	Leu	Glu	Ala	Leu	Ser	Ala	Ser	Leu	Gly	Thr	Arg	Gln		
	275						280					285					
Ala	Glu	Pro	Glu	Leu	Asp	Leu	Arg	Ser	Ile	Lys	Glu	Val	Asp	Glu	Ala		
	290					295					300						
Lys	Ala	Lys	Glu	Glu	Lys	Leu	Glu	Lys	Cys	Gly	Glu	Asp	Asp	Glu	Thr		
305					310					315					320		
Ile	Pro	Ser	Glu	Tyr	Arg	Leu	Lys	Pro	Ala	Thr	Asp	Lys	Asp	Gly	Lys		
				325					330						335		
Pro	Leu	Leu	Pro	Glu	Pro	Glu	Glu	Lys	Pro	Lys	Pro	Arg	Ser	Glu	Ser		
			340					345						350			
Glu	Leu	Ile	Asp	Glu	Leu	Ser	Glu	Asp	Phe	Asp	Arg	Ser	Glu	Cys	Lys		
			355				360					365					
Glu	Lys	Pro	Ser	Lys	Pro	Thr	Glu	Lys	Thr	Glu	Glu	Ser	Lys	Ala	Ala		
	370					375					380						
Ala	Pro	Ala	Pro	Val	Ser	Glu	Ala	Val	Ser	Arg	Thr	Ser	Met	Cys	Ser		
385					390					395					400		
Ile	Gln	Ser	Ala	Pro	Pro	Glu	Pro	Ala	Thr	Leu	Lys	Gly	Thr	Val	Pro		
				405					410						415		
Asp	Asp	Ala	Val	Glu	Ala	Leu	Ala	Asp	Ser	Leu	Gly	Lys	Lys	Glu	Ala		
			420					425						430			

	565		570		575
Met Gly Asp	Lys Val Lys Glu Lys Ala	Lys Ala Glu His Arg Asp Lys			
	580	585	590		
Leu Gly Glu	Arg Asp Asp Thr Ile Pro	Pro Glu Tyr Arg His Leu Leu			
	595	600	605		
Asp Asp Asn	Gly Gln Asp Lys Pro Val	Lys Pro Pro Thr Lys Lys Ser			
	610	615	620		
Glu Asp Ser	Lys Lys Pro Ala Asp Asp Gln Asp	Pro Ile Asp Ala Leu			
	625	630	635	640	
Ser Gly Asp	Leu Asp Ser Cys Pro Ser Thr	Glu Thr Ser Gln Asn			
	645	650	655		
Thr Ala Lys	Asp Lys Cys Lys Lys Ala Ala	Ser Ser Ser Lys Ala Pro			
	660	665	670		
Lys Asn Gly	Gly Lys Ala Lys Asp Ser Ala	Lys Thr Thr Glu Glu Thr			
	675	680	685		
Ser Lys Pro	Lys Asp Asp				
	690				

<210> 3
 <211> 399
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (399)

<400> 3	
tca ggc atg gat gct gct ttg gat gac tta ata gat act tta gga gga	48
Ser Gly Met Asp Ala Ala Leu Asp Asp Leu Ile Asp Thr Leu Gly Gly	
1 5 10 15	
cct gaa gaa act gaa gaa gaa aat aca acg tat act gga cca gaa gtt	96
Pro Glu Glu Thr Glu Glu Glu Asn Thr Thr Tyr Thr Gly Pro Glu Val	
20 25 30	
tca gat cca atg agt tcc acc tac ata gag gaa ttg ggt aaa aga gaa	144
Ser Asp Pro Met Ser Ser Thr Tyr Ile Glu Glu Leu Gly Lys Arg Glu	
35 40 45	
gtc aca att cct cca aaa tat agg gaa cta ttg gct aaa aag gaa ggg	192
Val Thr Ile Pro Pro Lys Tyr Arg Glu Leu Leu Ala Lys Lys Glu Gly	
50 55 60	
atc aca ggg cct cct gca gac tct tca aaa ccc ata ggg cca gat gat	240
Ile Thr Gly Pro Pro Ala Asp Ser Ser Lys Pro Ile Gly Pro Asp Asp	
65 70 75 80	
gct ata gac gcc ttg tca tct gac ttc acc tgt ggg tcg cct aca gct	288
Ala Ile Asp Ala Leu Ser Ser Asp Phe Thr Cys Gly Ser Pro Thr Ala	
85 90 95	
gct gga aag aaa act gaa aaa gag gaa tct aca gaa gtt tta aaa gct	336
Ala Gly Lys Lys Thr Glu Lys Glu Glu Ser Thr Glu Val Leu Lys Ala	
100 105 110	

cag tca gca ggg aca gtc aga agt gct gct cca ccc caa gag aag aaa 384
 Gln Ser Ala Gly Thr Val Arg Ser Ala Ala Pro Pro Gln Glu Lys Lys
 115 120 125

aga aag gtg gag aag 399
 Arg Lys Val Glu Lys
 130

<210> 4
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 4
 Ser Gly Met Asp Ala Ala Leu Asp Asp Leu Ile Asp Thr Leu Gly Gly
 1 5 10 15

Pro Glu Glu Thr Glu Glu Glu Asn Thr Thr Tyr Thr Gly Pro Glu Val
 20 25 30

Ser Asp Pro Met Ser Ser Thr Tyr Ile Glu Glu Leu Gly Lys Arg Glu
 35 40 45

Val Thr Ile Pro Pro Lys Tyr Arg Glu Leu Leu Ala Lys Lys Glu Gly
 50 55 60

Ile Thr Gly Pro Pro Ala Asp Ser Ser Lys Pro Ile Gly Pro Asp Asp
 65 70 75 80

Ala Ile Asp Ala Leu Ser Ser Asp Phe Thr Cys Gly Ser Pro Thr Ala
 85 90 95

Ala Gly Lys Lys Thr Glu Lys Glu Glu Ser Thr Glu Val Leu Lys Ala
 100 105 110

Gln Ser Ala Gly Thr Val Arg Ser Ala Ala Pro Pro Gln Glu Lys Lys
 115 120 125

Arg Lys Val Glu Lys
 130